```
ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA          50
M  A  L  E   Q  N  Q   S  T  D   Y  Y  Y  E   E  N  E

AATGAATGGC ACTTATGACT ACAGTCAATA TGAACTGATC TGTATCAAAG         100
 M  N  G   T  Y  D  Y   S  Q  Y   E  L  I   C  I  K  E

AAGATGTCAG AGAATTTGCA AAAGTTTTCC TCCCTGTATT CCTCACAATA         150
  D  V  R   E  F  A   K  V  F  L   P  V  F   L  T  I

GTTTTCGTCA TTGGACTTGC AGGCAATTCC ATGGTAGTGG CAATTTATGC         200
V  F  V  I   G  L  A   G  N  S   M  V  V  A   I  Y  A

CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC CTGAATTTGG         250
 Y  Y  K   K  Q  R  T   K  T  D   V  Y  I   L  N  L  A

CTGTAGCAGA TTTACTCCTT CTATTCACTC TGCCTTTTTG GGCTGTTAAT         300
  V  A  D   L  L  L   L  F  T  L   P  F  W   A  V  N

GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC         350
A  V  H  G   W  V  L   G  K  I   M  C  K  I   T  S  A

CTTGTACACA CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA         400
 L  Y  T   L  N  F  V   S  G  M   Q  F  L   A  C  I  S

GCATAGACAG ATATGTGGCA GTAACTAAAG TCCCCAGCCA ATCAGGAGTG         450
  I  D  R   Y  V  A   V  T  K  V   P  S  Q   S  G  V

GGAAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT         500
G  K  P  C   W  I  I   C  F  C   V  W  M  A   A  I  L

GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC AATGCTAGGT         550
 L  S  I   P  Q  L  V   F  Y  T   V  N  D   N  A  R  C

GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT         600
  I  P  I   F  P  R   Y  L  G  T   S  M  K   A  L  I

CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG         650
Q  M  L  E   I  C  I   G  F  V   V  P  F  L   I  M  G

GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA         700
 V  C  Y   F  I  T  A   R  T  L   M  K  M   P  N  I  K

AAATATCTCG ACCCCTAAAA GTTCTGCTCA CAGTCGTTAT AGTTTTCATT         750
  I  S  R   P  L  K   V  L  L  T   V  V  I   V  F  I

GTCACTCAAC TGCCTTATAA CATTGTCAAG TTCTGCCGAG CCATAGACAT         800
V  T  Q  L   P  Y  N   I  V  K   F  C  R  A   I  D  I

CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG         850
 I  Y  S   L  I  T  S   C  N  M   S  K  R   M  D  I  A

CCATCCAAGT CACAGAAAGC ATCGCACTCT TTCACAGCTG CCTCAACCCA         900
  I  Q  V   T  E  S   I  A  L  F   H  S  C   L  N  P

ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT         950
I  L  Y  V   F  M  G   A  S  F   K  N  Y  V   M  K  V

GGCCAAGAAA TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT        1000
 A  K  K   Y  G  S  W   R  R  Q   R  Q  S   V  E  E  F

TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT        1050
  P  F  D   S  E  G   P  T  E  P   T  S  T   F  S  I

TAAAGGTAAA ACTGCTCTGC CTTTTGCTTG GATACATATG AATGATGCTT        1100
- R  - N   C  S  A   F  C  L   D  T  Y  E   - C  F

TCCCCTCAAA TAAAACATCT GCCTTATTCT GAAAAAAAAA AAAAAAM          1147
 P  L  K   - N  I  C   L  I  L   K  K  K   K  K
```

FIG. 1

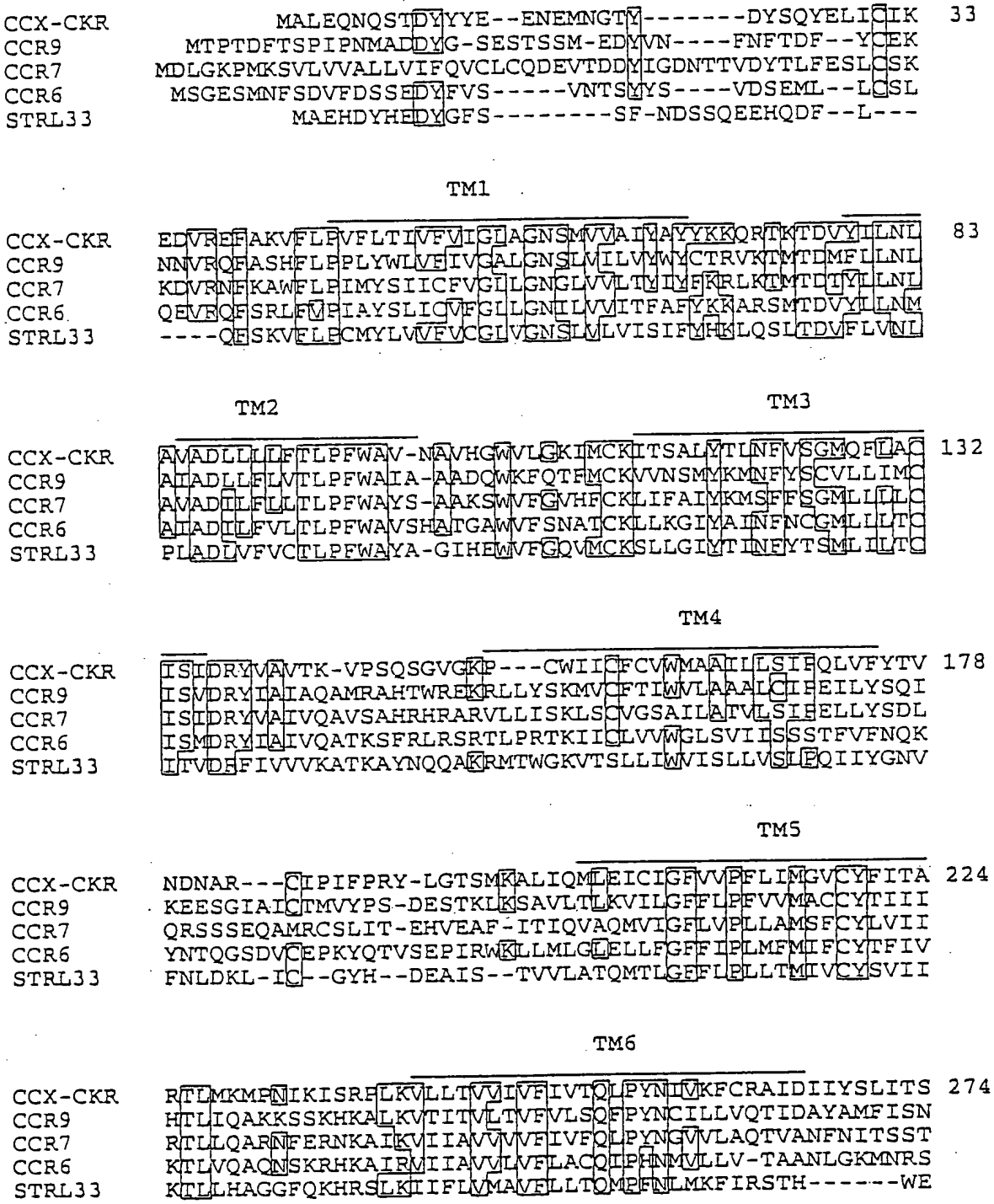

CCX-CKR MALEQNQSTDYYYE--ENEMNGTY-------DYSQYELICIK 33
CCR9 MTPTDFTSPIPNMADDYG-SESTSSM-EDYVN----FNFTDF--YCEK
CCR7 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSK
CCR6 MSGESMNFSDVFDSSEDYFVS-----VNTSMYS----VDSEML--LCSL
STRL33 MAEHDYHEDYGFS--------SF-NDSSQEEHQDF--L---
TM1
CCX-CKR EDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIVAYYKKQRTKTDVYILNL 83
CCR9 NNVRQFASHFLPPLYWLVFIVGALGNSLVILVVWYCTRVKTMTDMFLLNL
CCR7 KDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMTDTYLLNL
CCR6 QEVRQFSRLFVPIAYSLICVFGLLGNILVVITFAFYKKARSMTDVYLLNM
STRL33 ----QFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHKLQSLTDVFLVNL
TM2
TM3
CCX-CKR AVADLLLLFTLPFWAV-NAVHGWVLGKIMCKITSALYTLNFVSGMQFLAC 132
CCR9 AIADLLFLVTLPFWAIA-AADQWKFQTFMCKVVNSMYKMNFYSCVLLIMC
CCR7 AVADILFLLTLPFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGMLLLLC
CCR6 AIADILFVLTLPFWAVSHAIGAWVFSNAICKLLKGIYAINFNCGMLLLTC
STRL33 PLADLVFVCTLPFWAYA-GIHEWVFGQVMCKSLLGIYTINFYTSMLILTC
TM4
CCX-CKR ISIDRYVAVTK-VPSQSGVGKP---CWIICFCVWMAAILLSIPQLVFYTV 178
CCR9 ISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQI
CCR7 ISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDL
CCR6 ISMDRYIAIVQATKSFRLRSRTLPRTKIICLVVWGLSVIISSSTFVFNQK
STRL33 ITVDSFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNV
TM5
CCX-CKR NDNAR---CIPIFPRY-LGTSMKALIQMLEICIGFVVPFLIMGVCYFITA 224
CCR9 KEESGIAICTMVYPS-DESTKLKSAVLTLKVILGFFLPFVVMACCYTIII
CCR7 QRSSSEQAMRCSLIT-EHVEAF-ITIQVAQMVIGFLVPLLAMSFCYLVII
CCR6 YNTQGSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIV
STRL33 FNLDKL-IC--GYH--DEAIS--TVVLATQMTLGFFLPLLTMIVCYSVII
TM6
CCX-CKR RTLMKMPNIKISRPLKVLLTVVILVFIVTQLPYNIVKFCRAIDIIYSLITS 274
CCR9 HTLIQAKKSSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISN
CCR7 RTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSST
CCR6 KTLVQAQNSKRHKAIRVIIAVVLVFLACQIPHNMVLLV-TAANLGKMNRS
STRL33 KTLLHAGGFQKHRSLKIIFLVMAVFLLTQMPFNLMKFIRSTH------WE

FIG. 2A

TM7

```
CCX-CKR   CNMSKRMDIAIQVTESIALFHSCLNPILYVFMGASFKNYVMK--------V 317
CCR9      CAVSTNIDICFQVTQTLAFFHSCLNPVLYVFVGERFRRDLVKTLKNLGCI
CCR7      CELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCL
CCR6      CQSEKLIGYTKTVTEVLAFLHCCLNPVLYAFIGQKFRNYFLKILKDLWCV
STRL33    YYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL

CCX-CKR   AKKY--GSWRRQRQSVEEFPFDSEGP--TEPTSTFSI          350
CCR9      SQA-QWVSFTR----REGSLK-LSSMLLETTSGALSL
CCR7      SQE-QLRQWSS----CRHIRR-SSMSVEAETITTFSP
CCR6      RRKYKSSGFSCAGRYSENISRQTSETADNDNASSFTM
STRL33    P--Y--LGVSHQWKSSEDNSKTFSASHNVEATSMFQL
```

FIG. 2A
(CONTINUED)

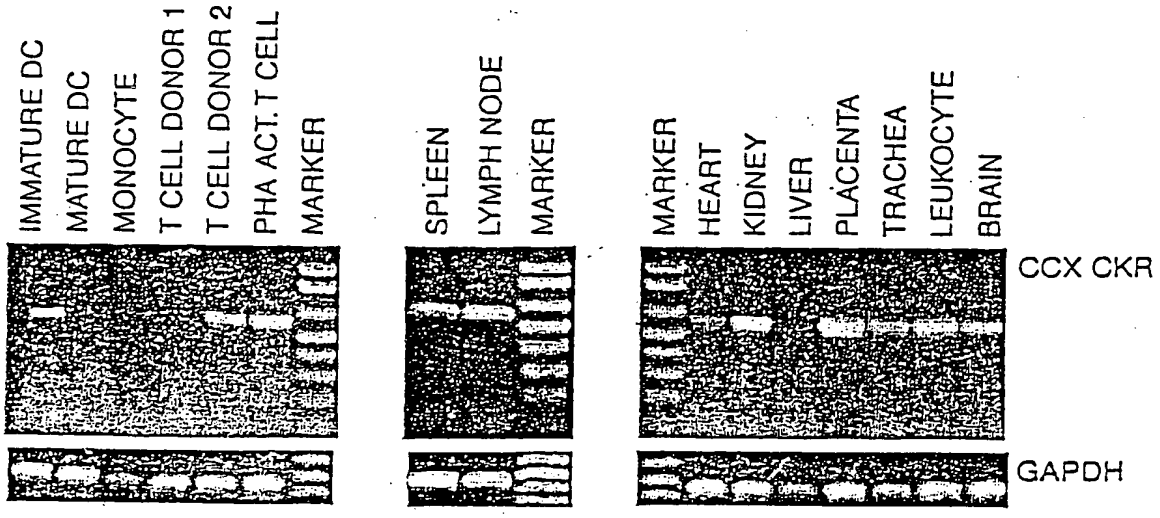


FIG. 2B

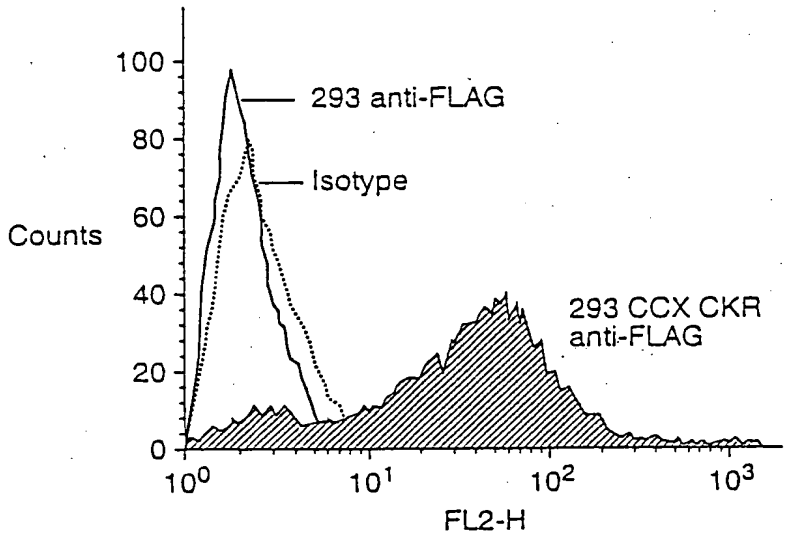

100
80
60
40
20
0
Counts
293 anti-FLAG
Isotype
293 CCX CKR
anti-FLAG
10^0
10^1
10^2
10^3
FL2-H

FIG. 2C

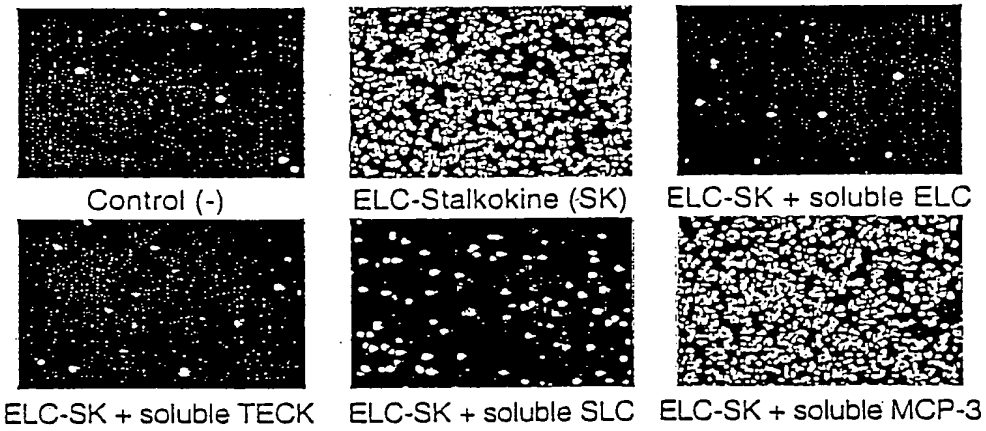

Control (-)
ELC-Stalkokine (SK)
ELC-SK + soluble ELC
ELC-SK + soluble TECK
ELC-SK + soluble SLC
ELC-SK + soluble MCP-3

FIG. 3A

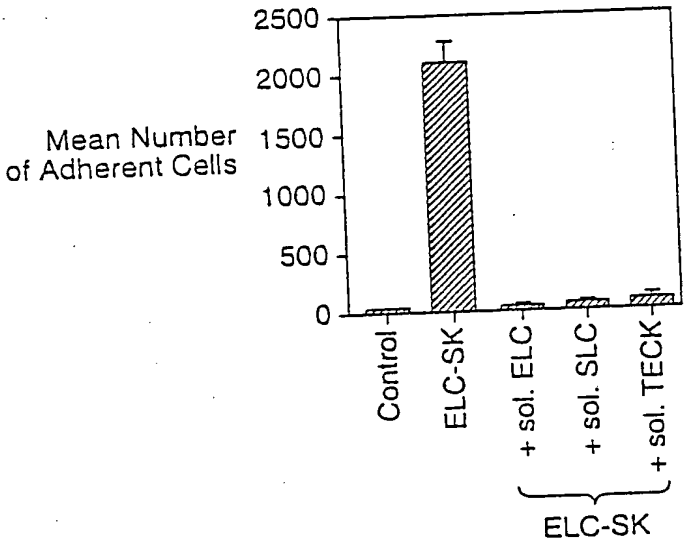

Mean Number of Adherent Cells
2500
2000
1500
1000
500
0
Control
ELC-SK
+ sol. ELC
+ sol. SLC
+ sol. TECK
ELC-SK

FIG. 3B

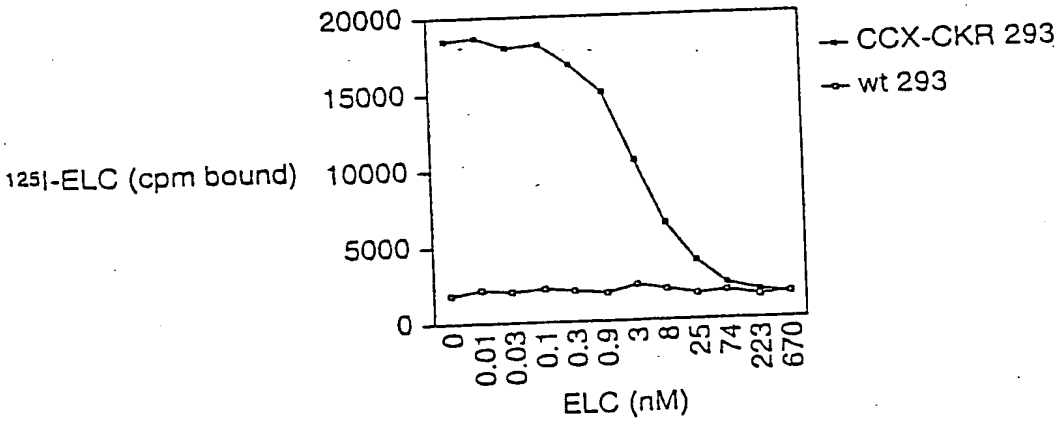

125I-ELC (cpm bound)
20000
15000
10000
5000
0
0
0.01
0.03
0.1
0.3
0.9
3
8
25
74
223
670
ELC (nM)
CCX-CKR 293
wt 293

FIG. 3C

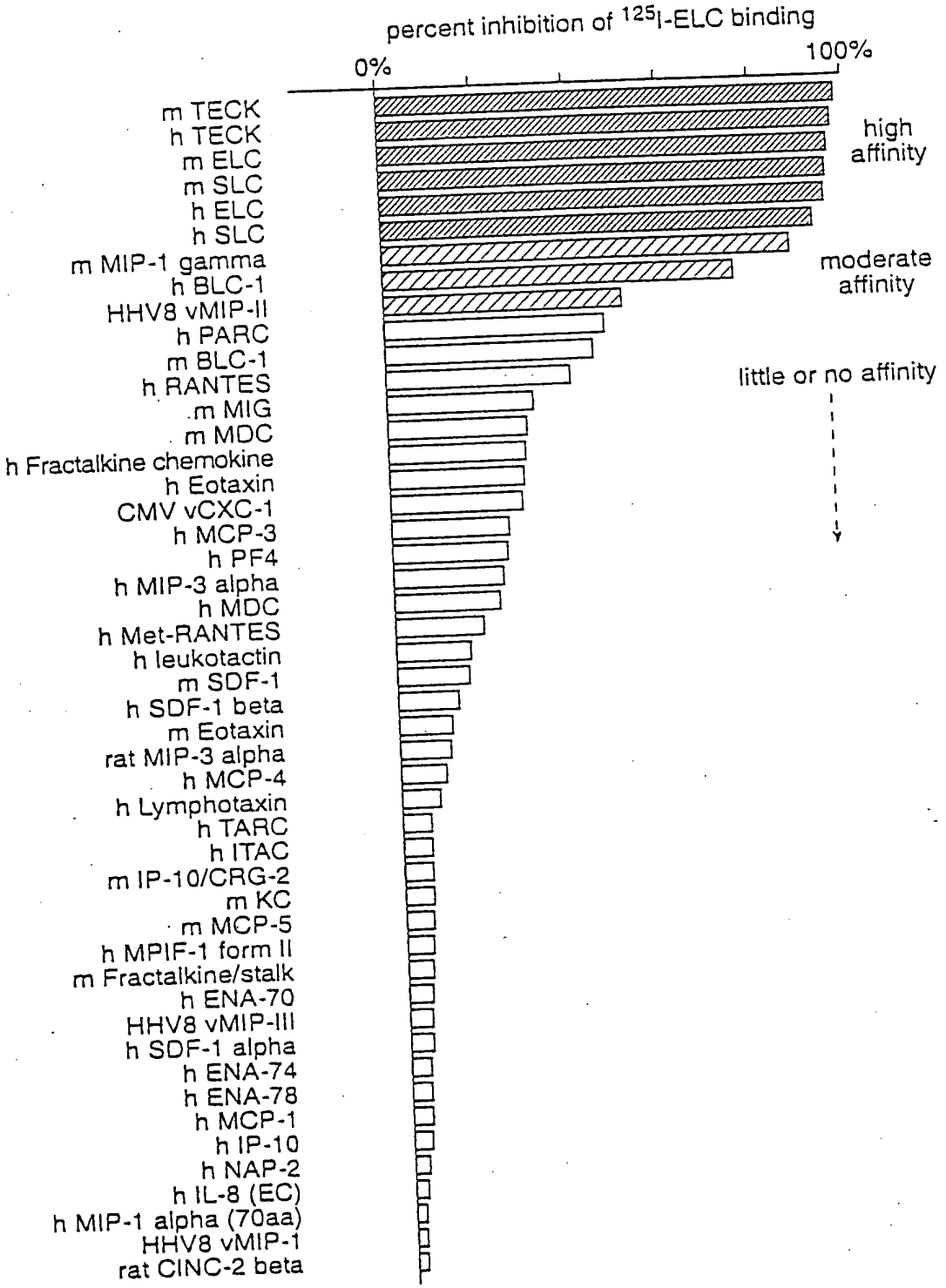

percent inhibition of ^{125}I-ELC binding
0%
100%
m TECK
h TECK
m ELC
m SLC
h ELC
h SLC
m MIP-1 gamma
h BLC-1
HHV8 vMIP-II
h PARC
m BLC-1
h RANTES
m MIG
m MDC
h Fractalkine chemokine
h Eotaxin
CMV vCXC-1
h MCP-3
h PF4
h MIP-3 alpha
h MDC
h Met-RANTES
h leukotactin
m SDF-1
h SDF-1 beta
m Eotaxin
rat MIP-3 alpha
h MCP-4
h Lymphotaxin
h TARC
h ITAC
m IP-10/CRG-2
m KC
m MCP-5
h MPIF-1 form II
m Fractalkine/stalk
h ENA-70
HHV8 vMIP-III
h SDF-1 alpha
h ENA-74
h ENA-78
h MCP-1
h IP-10
h NAP-2
h IL-8 (EC)
h MIP-1 alpha (70aa)
HHV8 vMIP-1
rat CINC-2 beta
high affinity
moderate affinity
little or no affinity

FIG. 4A

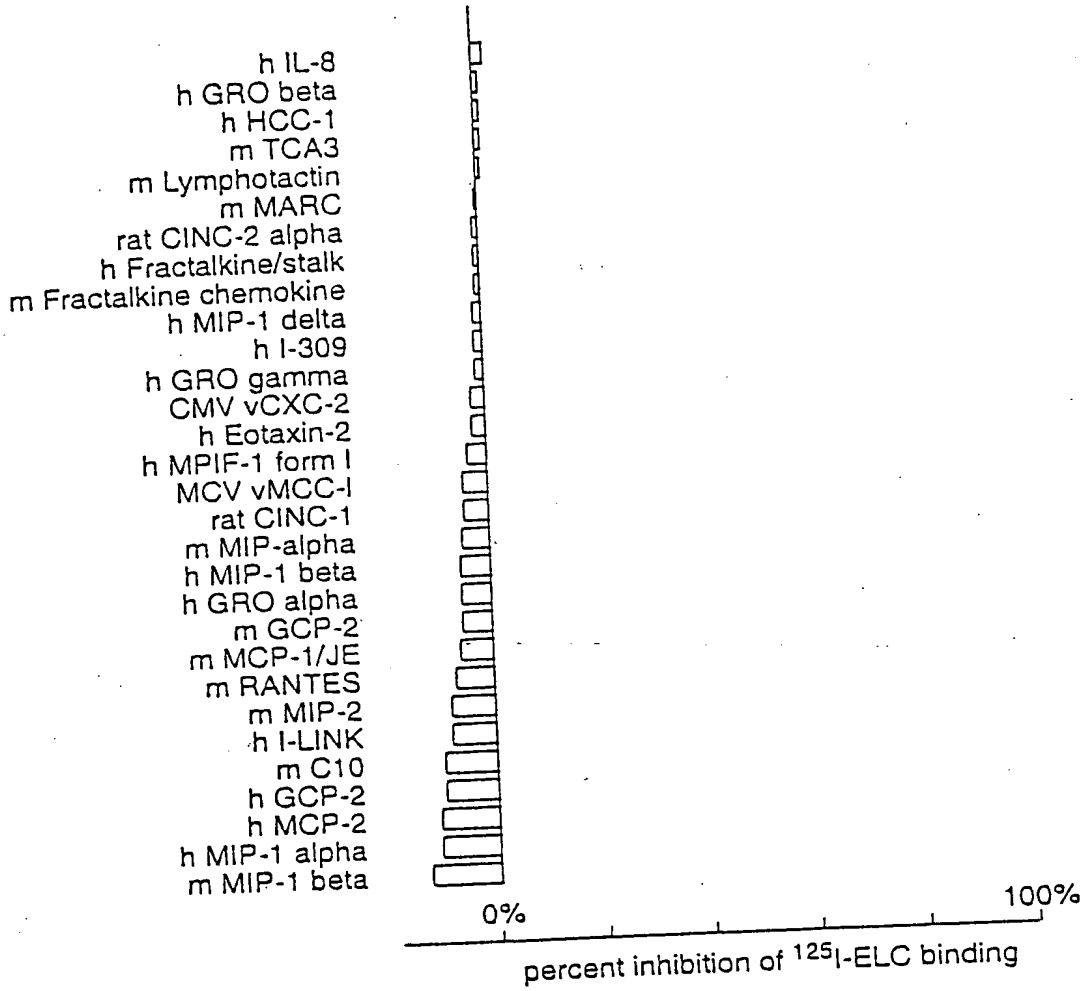
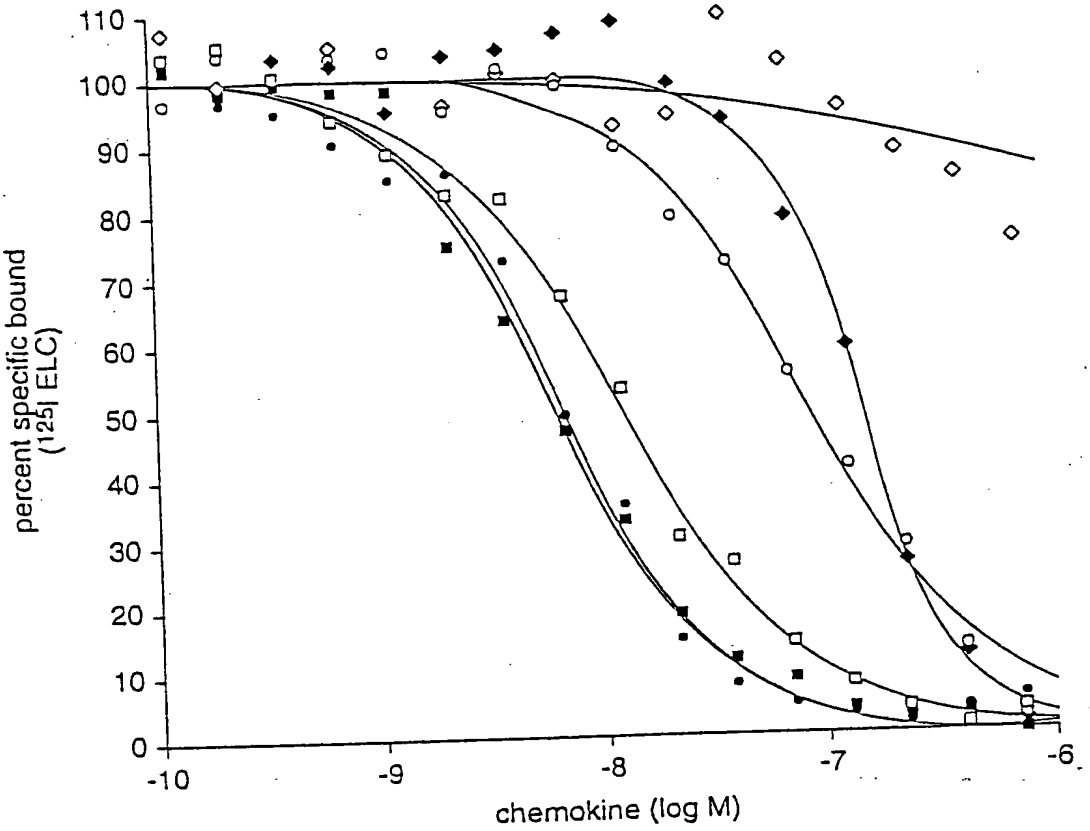


FIG. 4A
(CONTINUED)



human chemokines	IC-50	murine chemokines	IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
• h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B

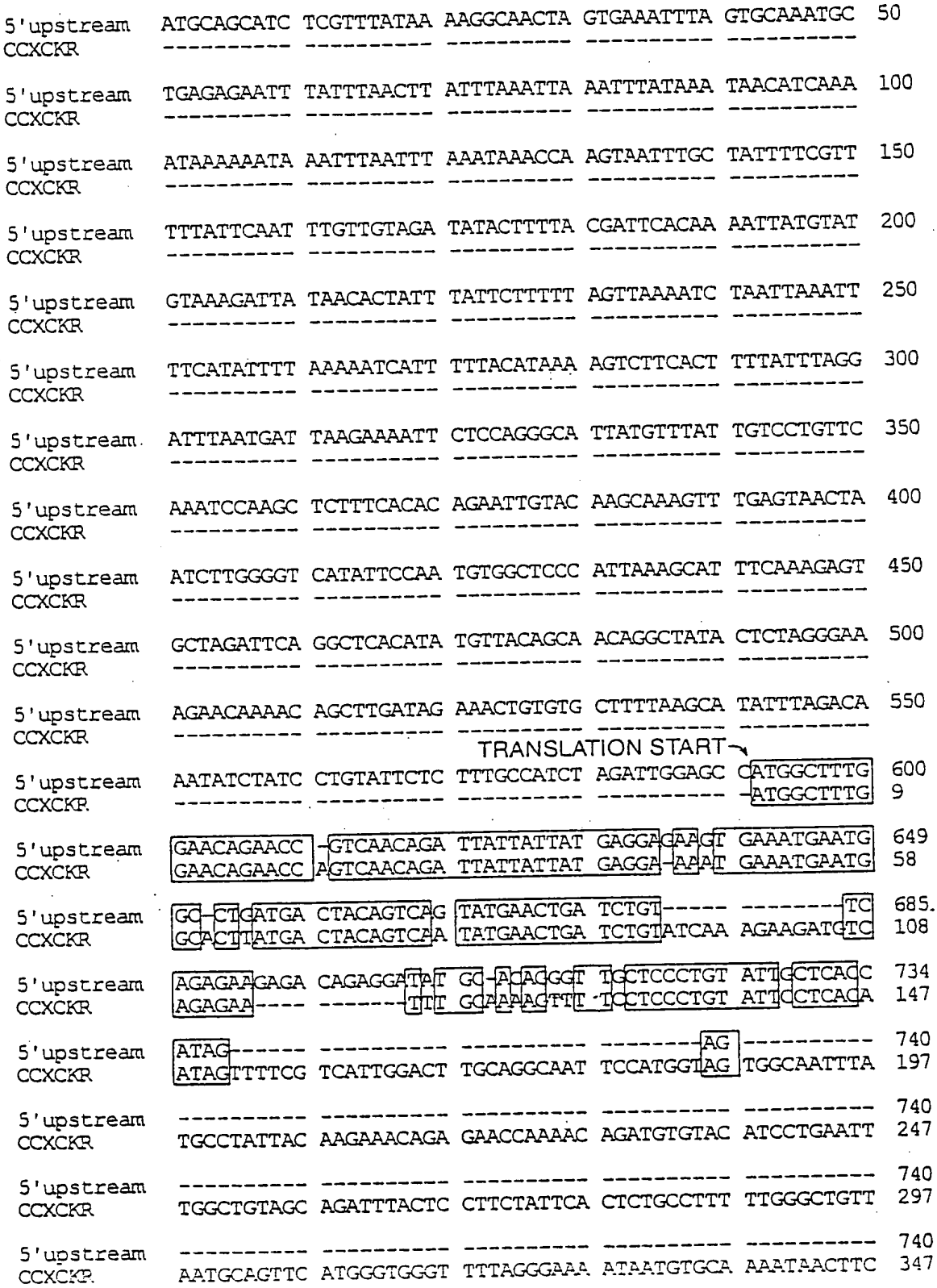

5'upstream ATGCAGCATC TCGTTTATAA AAGGCAACTA GTGAAATTTA GTGCAAATGC 50
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream TGAGAGAATT TATTTAACTT ATTTAAATTA AATTTATAAA TAACATCAAA 100
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream ATAAAAAATA AATTTAATTT AAATAAACCA AGTAATTTGC TATTTTCGTT 150
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream TTTATTCAAT TTGTTGTAGA TATACTTTTA CGATTCACAA AATTATGTAT 200
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream GTAAAGATTA TAACACTATT TATTCTTTTT AGTTAAAATC TAATTAAATT 250
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream TTCATATTTT AAAAATCATT TTTACATAAA AGTCTTCACT TTTATTTAGG 300
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream ATTTAATGAT TAAGAAAATT CTCCAGGGCA TTATGTTTAT TGTCCTGTTC 350
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream AAATCCAAGC TCTTTCACAC AGAATTGTAC AAGCAAAGTT TGAGTAACTA 400
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream ATCTTGGGGT CATATTCCAA TGTGGCTCCC ATTAAAGCAT TTCAAAGAGT 450
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream GCTAGATTCA GGCTCACATA TGTTACAGCA ACAGGCTATA CTCTAGGGAA 500
CCXCKR ---------- ---------- ---------- ---------- ----------
5'upstream AGAACAAAAC AGCTTGATAG AAACTGTGTG CTTTTAAGCA TATTTAGACA 550
CCXCKR ---------- ---------- ---------- ---------- ----------
TRANSLATION START
5'upstream AATATCTATC CTGTATTCTC TTTGCCATCT AGATTGGAGC CATGGCTTTG 600
CCXCKR ---------- ---------- ---------- ---------- -ATGGCTTTG 9
5'upstream GAACAGAACC -GTCAACAGA TTATTATTAT GAGGAGAAGT GAAATGAATG 649
CCXCKR GAACAGAACC AGTCAACAGA TTATTATTAT GAGGA-AAAT GAAATGAATG 58
5'upstream GC-CTCATGA CTACAGTCAG TATGAACTGA TCTGT----- --------TC 685.
CCXCKR GCACTTATGA CTACAGTCAA TATGAACTGA TCTGTATCAA AGAAGATGTC 108
5'upstream AGAGAAGAGA CAGAGGATAT GC-ACAGGT TGCTCCCTGT ATTGCTCACC 734
CCXCKR AGAGAA---- -------TTT GCAAAAGTTT TCCTCCCTGT ATTCCTCAGA 147
5'upstream ATAG------ ---------- ---------- --------AG---------- 740
CCXCKR ATAGTTTTCG TCATTGGACT TGCAGGCAAT TCCATGGTAG TGGCAATTTA 197
5'upstream ---------- ---------- ---------- ---------- ---------- 740
CCXCKR TGCCTATTAC AAGAAACAGA GAACCAAAAC AGATGTGTAC ATCCTGAATT 247
5'upstream ---------- ---------- ---------- ---------- ---------- 740
CCXCKR TGGCTGTAGC AGATTTACTC CTTCTATTCA CTCTGCCTTT TTGGGCTGTT 297
5'upstream ---------- ---------- ---------- ---------- ---------- 740
CCXCKR AATGCAGTTC ATGGGTGGGT TTTAGGGAAA ATAATGTGCA AAATAACTTC 347

FIG. 5

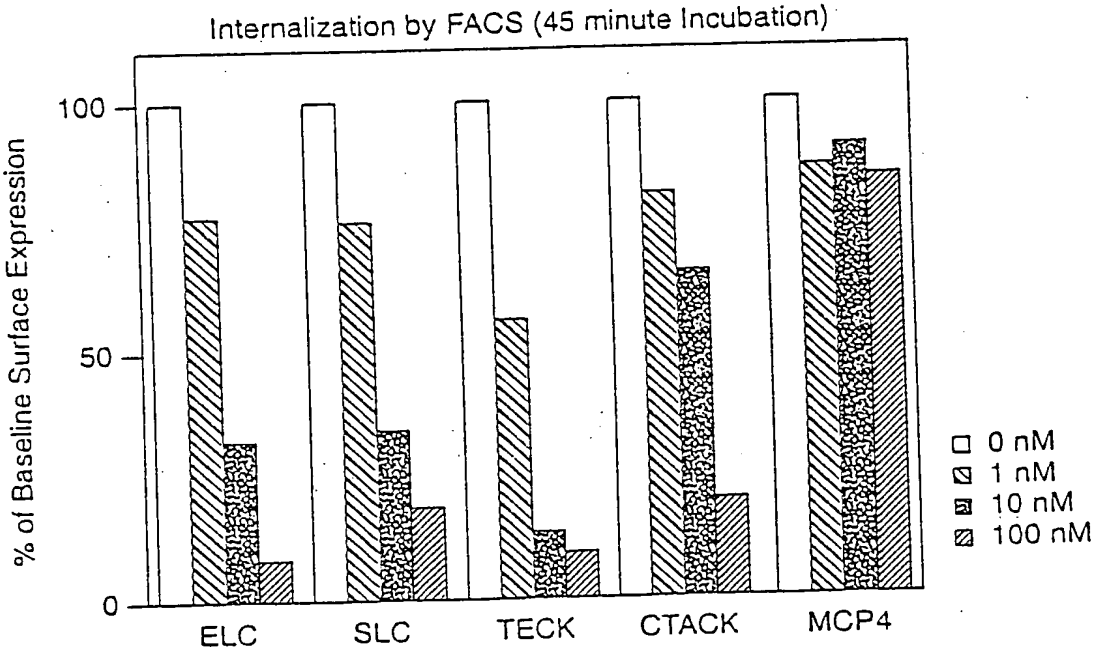

Internalization by FACS (45 minute Incubation)
% of Baseline Surface Expression
100
50
0
ELC
SLC
TECK
CTACK
MCP4
0 nM
1 nM
10 nM
100 nM

FIG. 6A

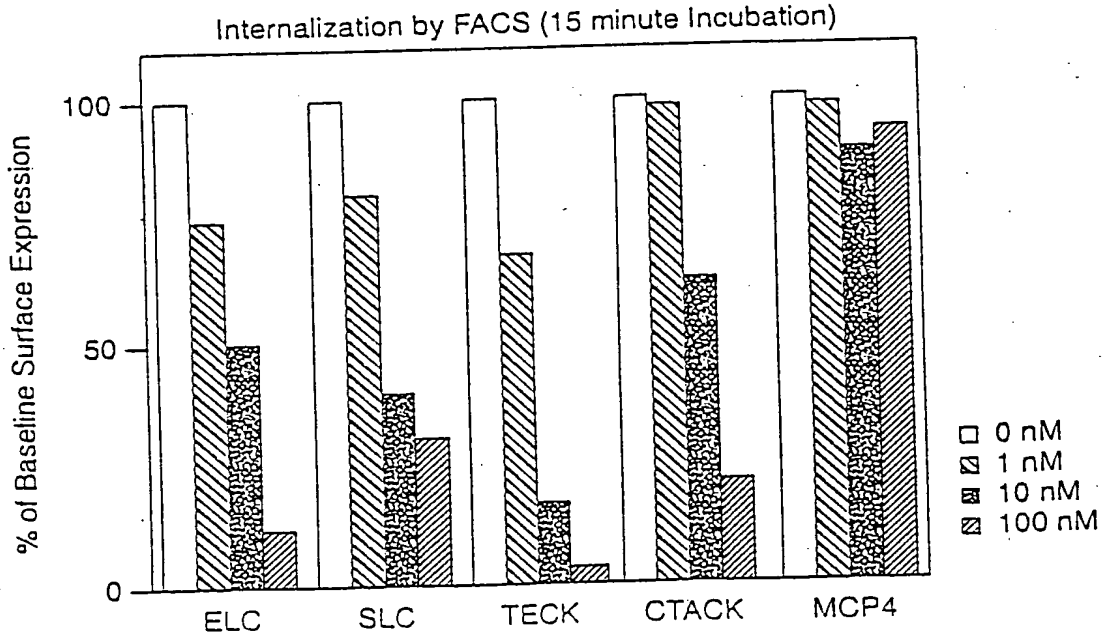

Internalization by FACS (15 minute Incubation)
% of Baseline Surface Expression
100
50
0
ELC
SLC
TECK
CTACK
MCP4
0 nM
1 nM
10 nM
100 nM

FIG. 6B